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OM protein - protein search, using sw model

Run on: February 18, 2004, 16:02:55 ; Search time 41 Seconds
(without alignments)
42.585 Million cell updates/sec

Title: US-09-846-342a-1_COPY_2_12
Perfect score: 58
Sequence: 1 GDFLAEGGVR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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21: /SIDSI1/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
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23: /SIDSI1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDSI1/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	16	17 AAR96194	Fibrinogen epitope
2	58	100.0	16	AAW04619	Fibrinopeptide A p
3	58	100.0	16	AAV57487	Antimicrobial pept
4	58	100.0	16	ABV56219	Vascular dementia-
5	58	100.0	16	ABV52337	Human ARI-118 try
6	58	100.0	16	ABV51959	Fibrinectin fragme
7	58	100.0	16	ABG73668	Linear HIV-1 gp120
8	58	100.0	16	ABG78799	Multiple sclerosis
9	58	100.0	16	ABG69911	Rabbit platelet mi

10	58	100.0	16	23	ABG70000	Antimicrobial pept
11	58	100.0	16	24	ABP60640	Fibrinopeptide A.
12	58	100.0	16	24	ABP60019	Biopolymer disease
13	58	100.0	17	22	AAR96184	Fibrinogen epitope
14	58	100.0	17	22	AAR91960	Fibrinectin fragme
15	58	100.0	17	24	ABU09101	Alpha fibrinogen b
16	58	100.0	17	24	AAE34820	Staphylococcus epi
17	58	100.0	18	17	AAR96193	Fibrinogen epitope
18	58	100.0	19	17	AAR96192	Fibrinogen epitope
19	58	100.0	20	17	AAR96191	Fibrinogen epitope
20	58	100.0	20	17	AAV57488	Antimicrobial pept
21	58	100.0	20	23	ABG69912	Rabbit platelet mi
22	58	100.0	20	24	AAO27081	Fibrinogen E fragm
23	58	100.0	20	24	AAO27084	Fibrinogen E fragm
24	58	100.0	20	24	AAO27085	Fibrinogen E fragm
25	58	100.0	20	24	AAO27086	Fibrinogen E fragm
26	58	100.0	21	17	AAR96183	Fibrinogen epitope
27	58	100.0	22	17	AAV90276	Antigen probe for
28	58	100.0	22	17	AAR96182	Fibrinogen epitope
29	58	100.0	22	17	AAR96190	Fibrinogen epitope
30	58	100.0	24	23	AAO21112	Anti-angiogenic al
31	58	100.0	24	23	AAO21113	Anti-angiogenic al
32	58	100.0	24	23	AAO21114	Anti-angiogenic al
33	58	100.0	24	23	AAO21115	Anti-angiogenic al
34	58	100.0	24	23	AAO21119	Anti-angiogenic al
35	58	100.0	24	24	AAO27090	Fibrinogen E fragm
36	58	100.0	24	24	AAO27094	Fibrinogen E fragm
37	58	100.0	24	24	AAO27095	Fibrinogen E fragm
38	58	100.0	24	24	AAO27096	Fibrinogen E fragm
39	58	100.0	24	24	AAO27097	Fibrinogen E fragm
40	58	100.0	25	23	AAV79318	Lupus peptide, Ci-
41	58	100.0	25	23	AAV51100	Peptide used in pu
42	58	100.0	28	12	AAR11166	Hirulog-33. Synth
43	58	100.0	28	23	AAO21122	Fibrinogen E alpha
44	58	100.0	78	23	AAO14005	Human fibrinogen E
45	58	100.0	360	21	AAB54135	Human pancreatic c

ALIGNMENTS

RESULT 1

AAR96194
ID AAR96194 standard; peptide; 16 AA.

XX AAR96194;

AC AAR96194;

DT 19-DEC-1996 (first entry)

XX Fibrinogen epitope probe, represents alpha chain residues 1-16.

XX Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
chronic obstructive pulmonary disease; myelogenous leukaemia;
infantile respiratory distress syndrome; gout;
adult respiratory distress syndrome.

XX Homo sapiens.

XX OS

XX WO9614580-A1.

XX 17-MAY-1996.

XX 03-NOV-1995; 95WO-US13794.

XX 06-JUN-1995; 95US-0469141.

XX 07-NOV-1994; 94US-0335524.

XX (MERI) MERCK & CO INC.

XX Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

XX WPI; 1996-251888/25.
XX
XX New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
XX Example 5; Page 42; 109pp; English.
XX
XX The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complementary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC bronchoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
XX SQ Sequence 16 AA;
SQ
Query Match 100.0%; Score 58; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
Db |||||
6 GDFLAEGGGVR 16
RESULT 2
AAW04619
ID AAW04619 standard; peptide; 16 AA.
XX
XX AC AAW04619;
XX
XX 13-AUG-1997 (first entry)
XX
XX Fibrinopeptide A peptide for mass spectrometry analysis.
XX
XX Mass spectrometry; polymer analysis; biopolymer analysis.
XX
XX Synthetic.
XX
XX WO9636986-A1.
XX
XX 21-NOV-1996.
XX
XX 17-MAY-1996; 96WO-US07146.
XX
XX 19-MAY-1995; 95US-0447175.
XX
XX 19-MAY-1995; 95US-0446055.
XX
XX (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
XX Patterson DH, Tarr GE;
XX
XX WPI; 1997-012308/01.
XX
XX Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
PT etc. - by obtaining mass to charge ratios of polymer fragments,
PT pref. using mass spectrometer, and performing statistical analysis
XX
XX Example 2; Page 32; 86pp; English.
XX
XX A method of obtaining sequence information about a polymer (e.g. DNA,
CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
CC comprising monomers of known mass has been claimed. The present
CC sequence represents a fibrinopeptide A peptide, and was used as

CC an example as a digestion before analysis by mass spectrometry,
CC using this novel on-plate strategy. Total sequence information
CC from a nine well digestion can be represented in a single digestion or
CC it is often derived from two or more wells. The methods, apparatus and
CC kit (claimed) can be used for the analysis of polymers, particularly
CC biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
CC and carbohydrates. It provides a rapid, automated and cost effective
CC sequencing of polymers, with a statistical certainty.
XX
XX SQ Sequence 16 AA;
SQ
Query Match 100.0%; Score 58; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
Db |||||
6 GDFLAEGGGVR 16
RESULT 3
AAV57487
ID AAV57487 standard; Peptide; 16 AA.
XX
XX AC AAV57487;
XX
XX 25-FEB-2000 (first entry)
XX
XX DE Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
XX
XX PN WO9942119-A1.
XX
XX PD 26-AUG-1999.
XX
XX PF 17-FEB-1999; 99WO-US03350.
XX
XX PR 18-FEB-1998; 98US-0025319.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi -
XX
XX PS Disclosure; Page 120; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXBXB, BXZXB, BXZXBXB and BXZXBXB2; and
CC (b) a second peptide template XBXX and their derivatives selected from
CC the group consisting of XBZXBXB, XBZXBXB, BXZXBXB, and
CC XBZXBXBXBXBXB; where B = at least one positively charged amino acid;
CC X = at least one non-polar hydrophobic amino acid; Z = at least one
CC aromatic amino acid, and where B, X and Z may be separated by one or
CC more other amino acids. The peptides can be used to treat bacterial and
CC fungal infections. The peptides also increase the antimicrobial activity
CC of neutrophils. The peptides overall effect cellular disruption and
CC rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent
CC sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 16 AA;
SQ

Query Match 100.0%; Score 58; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11
 |
 Db 6 GDFLAEGGGVR 16

RESULT 4

ABB56219
 ID ABB56219 standard; Peptide; 16 AA.

XX AC ABB56219;
 XX DT 15-FEB-2002 (first entry)
 XX DE Vascular dementia-associated protein isoform (VPI) 419.
 XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 XX OS diagnosis; prognosis; gene therapy.

XX OS Homo sapiens.

XX PN WO200169261-A2.

XX PD 20-SEP-2001.

XX PF 14-MAR-2001; 2001WO-GB01106.

XX PR 15-MAR-2000; 2000GB-0006285.

XX PR 24-NOV-2000; 2000GB-0028734.

XX PR 28-NOV-2000; 2000US-0724391.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C;

XX DR WPI; 2001-557937/62.

XX PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD -

XX PS Claim 6; Page 39; 151pp; English.

XX CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for
 CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 58; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11
 |
 Db 6 GDFLAEGGGVR 16

RESULT 5

ABB52337
 ID ABB52337 standard; Peptide; 16 AA.

XX AC ABB52337;

XX DT 08-FEB-2002 (first entry)

XX DE Human API-118 tryptic digest peptide #2.

XX KW Human; neuroprotective; neurotropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN WO200175454-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US10908.

XX PR 03-APR-2000; 2000US-194504P.

XX PR 28-NOV-2000; 2000US-253647P.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 (PFIZ) PFIZER INC.

XX PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;

XX PI Potter KM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX PI Townsend RR, White F, Williams SA;

XX DR WPI; 2001-639384/73.

XX PT Screening for Alzheimer's disease in a mammal, by making
 PT two-dimensional array of a feature whose relative abundance correlates
 PT with disease, and comparing with abundance of the feature in samples of
 PT healthy persons -

XX PS Example; Page 33; 162pp; English.

XX CC The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the APIs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the APIs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 58; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11
 |
 Db 6 GDFLAEGGGVR 16

RESULT 6

AAB91959
 ID AAB91959 standard; Peptide; 16 AA.

XX AC AAB91959;

XX DT 22-JUN-2001 (first entry)

XX

DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1135.
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT -
XX
XX Disclosure; Page 567; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 58; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
Db 6 GDFLAEGGGVR 16
RESULT 7
ABG73668
ID ABG73668 standard; Peptide; 16 AA.
XX ABG73668;
XX
DT 11-MAR-2003 (first entry)
XX
DE Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.
XX
KW gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
KW HIV infection.

XX Human immunodeficiency virus type 1.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified_base /note= "residue can be modified with
FT beta-D-GlcNAc-(1-4)beta-D-GlcNAc"
XX
XX DE10113042-A1.
XX 26-SEP-2002.
XX 09-MAR-2001; 2001DE-1013042.
XX 09-MAR-2001; 2001DE-1013042.
XX (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
XX Schreiber M, Seifert A, Meyer B;
XX WPI; 2002-752120/82.
XX Identifying compounds that modify interaction of gp120 and
PT co-receptors, useful potentially for treating human immune deficiency
PT virus infection, also new peptides -
XX
XX Claim 10; Page 56; 68pp; German.
XX
XX This invention describes novel substances that modify the interaction
CC between the gp120 protein of human immunodeficiency virus (HIV), or its
CC fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
CC transmembrane receptors for HIV. The method comprises (a) immobilizing a
CC ligand for the co-receptor on a gold surface; (b) contacting the ligand
CC with suspended cells that express the co-receptor; and (c) determining
CC interaction by measuring the refractive index (RI) by plasmon resonance.
CC The procedure is repeated using cells that have been incubated with a
CC test compound, and this is identified if RI is lower for cells
CC preincubated with it. The ligand is a linear or cyclic (glyco)peptide
CC that includes the amino acid sequence of an HIV V3 loop (including
CC flanking Cys). The products of the invention have virucide and anti-HIV
CC (human immunodeficiency virus) activity and are useful for prevention
CC and/or treatment of HIV infection. This sequence represents a linear
CC HIV-1 gp120 V3-loop derived peptide ligand described in the disclosure
CC of the invention.
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 58; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
Db 6 GDFLAEGGGVR 16
RESULT 8
ABG78799
ID ABG78799 standard; Peptide; 16 AA.
XX
XX ABG78799;
AC
XX
DT 29-NOV-2002 (first entry)
XX
XX Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.
XX Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;
KW human; multiple sclerosis-associated protein isoform; MSF1;
KW antiinflammatory; neuroprotective.
XX
XX Homo sapiens.
XX

PN WO200259604-A2.
 PD 01-AUG-2002.
 XX 25-JAN-2002; 2002WO-GB00330.
 XX 26-JAN-2001; 2001US-264404P.
 PR 20-NOV-2001; 2001US-331647P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMAC, Perekh RB, Rohlf C;
 FI WPI; 2002-599812/64.
 XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.
 XX determining the stage or severity of MS, comprises detecting the
 PT presence of MS-associated features or protein isoforms by 2-dimensional
 PT electrophoresis
 XX
 XX Disclosure; Page 32; 128pp; English.

CC This invention relates to a novel method for screening or diagnosing
 CC multiple sclerosis (MS) in a subject to determine the stage or severity
 CC of MS, to identify a subject at risk of developing MS or to monitor the
 CC effect of a therapy administered. The method comprises analysing a
 CC sample body fluid from the subject by two-dimensional electrophoresis
 CC and detecting the presence of multiple sclerosis-associated features
 CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).
 CC The MSF's of the invention correspond to spots identified on a 2D gel
 CC these proteins may have antiinflammatory or neuroprotective activity.
 CC The methods of the invention and the compositions are useful for
 CC clinical screening, diagnosis and treatment of MS, for monitoring the
 CC effectiveness of MS treatment, for selecting participants in clinical
 CC trials, for identifying patients most likely to respond to a particular
 CC therapeutic treatment and for screening and developing drugs for
 CC treatment of MS. Agents that modulate the expression or activity of an
 CC MSPI are useful for treating MS, for preventing or delaying the onset or
 CC development of MS, to prevent or delay the progression of MS, or to
 CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding
 CC an MSPI, MSPI-related polypeptide, or their fragments are useful for
 CC promoting MSPI function by gene therapy. The present sequence represents
 CC a human multiple sclerosis associated feature tryptic digest
 CC peptide of the invention.

XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 58; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11
 |||||
 Db 6 GDFLAEGGGVR 16

RESULT 9
 ABG69911
 ID ABG69911 standard; Peptide; 16 AA.
 XX AC ABG69911;
 XX 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #23.
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 XX bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance;
 XX rabbit; mutant; mutein.
 OS Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.
 PN 18-JUL-2002.
 PD 24-AUG-2001; 2001WO-US41877.
 XX 25-AUG-2000; 2000US-0648816.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 FI WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment
 XX of infections caused by organisms, such as bacteria and fungi,
 PT exhibiting multiple antibiotic resistance
 XX
 XX Disclosure; Page 135; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of
 CC 5-150 amino acids containing a 7-13 amino acid core sequence
 CC (derived from PMP-1 and PMP-2, platelet microbicidal protein), and
 CC retromers, truncations, extensions, combinations, fusions and their
 CC derivatives. The possible structures are fully described in the
 CC specification. Also included are (1) an antimicrobial peptide composition
 CC for direct activity or for potentiating antimicrobial agents active
 CC against organisms such as bacteria and fungi comprising a peptide of
 CC 13-74 containing an amino acid core sequence selected from truncations of
 CC the peptides described above, and retromers, extensions, combinations and
 CC fusions; and (2) antimicrobial peptides for potentiating antimicrobial
 CC activity of leukocytes against organisms such as bacteria and fungi.
 CC The antimicrobial peptides are useful as individual antimicrobial
 CC agents, specifically against bacteria and fungi, agents in combination
 CC with other antimicrobials, agents that enhance, potentiate or restore
 CC efficacy of conventional antimicrobials, agents that enhance the
 CC antimicrobial functions of leukocytes, as disinfectants or
 CC preservatives for use in foods and cosmetics and as agents to improve
 CC efficiency of molecular biology techniques. Antimicrobial peptides of
 CC prior art have generally been considered to have undesirable toxicity,
 CC immunogenicity and short half-lives due to biodegradation. The peptides
 CC of the present invention are based upon natural antimicrobial peptides
 CC that have potent and broad spectrum activity against pathogens exhibiting
 CC multiple antibiotic resistance. They exhibit lower inherent mammalian
 CC cell toxicities and overcome problems of toxicity, immunogenicity, and
 CC shortness of duration of effectiveness due to biodegradation, retaining
 CC activity in plasma and serum. The present sequence is a rabbit PMP
 CC based antimicrobial peptide.

XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 58; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11
 |||||
 Db 6 GDFLAEGGGVR 16

RESULT 10
 ABG70000
 ID ABG70000 standard; Peptide; 16 AA.
 XX AC ABG70000;
 XX 21-OCT-2002 (first entry)
 XX Antimicrobial peptide CS-FBP.
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 XX Synthetic.

KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance.
 XX Unidentified.
 XX WO200255554-A2.
 XX 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US41877.
 XX 25-AUG-2000; 2000US-0648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment
 XX of infections caused by organisms, such as bacteria and fungi,
 XX exhibiting multiple antibiotic resistance -
 XX Disclosure; Page 18; 22pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of
 XX 5-150 amino acids containing a 7-13 amino acid core sequence
 XX (derived from PMP-1 and PMP-2, platelet microbicidal protein), and
 XX retromers, truncations, extensions, combinations, fusions and their
 XX derivatives. The possible structures are fully described in the
 XX specification. Also included are (1) an antimicrobial peptide composition
 XX for direct activity or for potentiating antimicrobial agents active
 XX against organisms such as bacteria and fungi comprising a peptide of
 XX 13-74 containing an amino acid core sequence selected from truncations of
 XX the peptides described above, and retromers, extensions, combinations and
 XX fusions; and (2) antimicrobial peptides for potentiating antimicrobial
 XX activity of leukocytes against organisms such as bacteria and fungi.
 XX The antimicrobial peptides are useful as individual antimicrobial
 XX agents, specifically against bacteria and fungi, agents in combination
 XX with other antimicrobials, agents that enhance, potentiate or restore
 XX efficacy of conventional antimicrobials, agents that enhance the
 XX antimicrobial functions of leukocytes, as disinfectants or
 XX preservatives for use in foods and cosmetics and as agents to improve
 XX efficiency of molecular biology techniques. Antimicrobial peptides of
 XX prior art have generally been considered to have undesirable toxicity,
 XX immunogenicity and short half-lives due to biodegradation. The peptides
 XX of the present invention are based upon natural antimicrobial peptides
 XX that have potent and broad spectrum activity against pathogens exhibiting
 XX multiple antibiotic resistance. They exhibit lower inherent mammalian
 XX cell toxicities and overcome problems of toxicity, immunogenicity, and
 XX shortness of duration of effectiveness due to biodegradation, retaining
 XX activity in plasma and serum. The present sequence is an antimicrobial
 XX peptide detailed in the disclosure but specifically excluded from
 XX the scope of the invention.
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 58; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDFLAEGGGVR 11
 |||||
 Db 6 GDFLAEGGGVR 16
 RESULT 11
 ABP60640
 ID ABP60640 standard; peptide; 16 AA.
 XX
 AC ABP60640;
 XX

DT 28-MAR-2003 (first entry)
 XX Fibrinopeptide A.
 DE Fibrinopeptide A.
 KW Fibrinopeptide A; N-terminus; protein identification.
 XX Unidentified.
 OS WO200295419-A2.
 PN 28-NOV-2002.
 XX 20-MAY-2002; 2002WO-US16247.
 XX 23-MAY-2001; 2001US-0863786.
 PR 20-DEC-2001; 2001US-343019P.
 XX (AMSH) AMERSHAM BIOSCIENCES AB.
 XX (PROC) PROCTER & GAMBLE CO.
 PA Bhikhabhai R, Liminga M, Maloisel J, Palmgren R, Keough TW;
 PI Youngquist RS, Vaughn HL, Yelm KE;
 XX WPI; 2003-175111/17.
 XX Identification of polypeptide useful in proteomics, involves
 XX derivatizing N-terminus or N-termini of polypeptide with acidic
 XX reagent containing sulfonyl or sulfonic acid moiety coupled to
 XX activated ester moiety -
 XX Example 3; Page 29; 90pp; English.
 XX The invention relates to a novel method for the identification of a
 XX polypeptide involving a step of derivatizing the N-terminus of the
 XX polypeptide or the N-termini of one or more polypeptides with acidic
 XX reagent containing a sulfonyl or sulfonic acid moiety coupled to an
 XX activated ester moiety, analysing the derivative using mass spectrometry
 XX and interpreting the resulting fragmentation pattern. The present
 XX sequence represents Fibrinopeptide A, used in example 3 of the invention.
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 58; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDFLAEGGGVR 11
 |||||
 Db 6 GDFLAEGGGVR 16
 RESULT 12
 ABP60019
 ID ABP60019 standard; peptide; 16 AA.
 XX
 AC ABP60019;
 XX
 XX 24-FEB-2003 (first entry)
 XX Biopolymer disease specific marker.
 DE Biopolymer; disease specific marker; marker; myocardial infarction;
 KW alpha fibrinogen.
 XX Homo sapiens.
 OS WO200288716-A2.
 PN 07-NOV-2002.
 PD 25-APR-2002; 2002WO-CA00577.
 XX 30-APR-2001; 2001US-0845765.
 PR

XX PA (SYNX-) SYN.X PHARMA INC.

XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX DR WPI; 2003-111905/10.

XX PT New biopolymer marker or its analyte, useful for determining the

XX PT presence or absence of at least one particular disease state, such as

XX PT myocardial infarction -

XX PS Claim 1; Page 28; 28pp; English.

XX CC The invention relates to a biopolymer disease specific marker. The

XX CC biopolymer marker is useful in indicating at least one particular disease

XX CC state, such as myocardial infarction. The method is useful for evidencing

XX CC and categorising at least one biopolymer marker sequence to determine the

XX CC presence or absence of at least one disease state. This marker is

XX CC characterised as an alpha fibrinogen having a molecular weight of 1518

XX CC daltons. The current sequence represents the biopolymer disease specific

XX CC marker of the invention.

XX S Sequence 16 AA;

Query Match 100.0%; Score 58; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11

Db 6 GDFLAEGGGVR 16

RESULT 13

AAR96184

ID AAR96184 standard; peptide; 17 AA.

XX AC AAR96184;

XX DT 19-DEC-1996 (first entry)

XX DE Fibrinogen epitope probe, represents alpha chain residues 5-21.

XX KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;

XX KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;

XX KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;

XX KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;

XX KW chronic obstructive pulmonary disease; myelogenous leukaemia;

XX KW infantile respiratory distress syndrome; gout;

XX KW adult respiratory distress syndrome.

XX OS Homo sapiens.

XX PN WO9614580-A1.

XX PD 17-MAY-1996.

XX PF 03-NOV-1995; 95WO-US13794.

XX PR 06-JUN-1995; 95US-0469141.

XX PR 07-NOV-1994; 94US-0335524.

XX PA (MERI) MERCK & CO INC.

XX PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

XX DR WPI; 1996-251888/25.

XX PT New isolated fibrinogen derived cleavage products - used for

XX PT detection of leukocyte elastase activity in disease diagnosis and

XX PT for evaluating elastase inhibitors

XX PS Example 5; Page 41; 109pp; English.

XX CC The sequences given in AAR96182-94 represent antigenic probes derived

XX CC from the first 21 amino acids of human fibrinogen. These probes are

XX CC used to determine antibody titre against other fibrinogen cleavage

XX CC products. The monospecific antibodies may be used to assay for the

XX CC formation of complementary cleavage product antigens or epitopes in

XX CC whole blood or other body fluids, peritoneal fluid, sputum or

XX CC bronchoalveolar lavage fluid. The assay for cleavage products is

XX CC dependent upon the presence of HLE in the sample. This assay can also

XX CC be used for the evaluation of HLE inhibitors. The antibodies may be

XX CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary

XX CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive

XX CC pulmonary disease, bronchiectasis, adult or infantile respiratory

XX CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.

XX S Sequence 17 AA;

Query Match 100.0%; Score 58; DB 17; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGGVR 11

Db 2 GDFLAEGGGVR 12

RESULT 14

AAB91960

ID AAB91960 standard; Peptide; 17 AA.

XX AC AAB91960;

XX DT 22-JUN-2001 (first entry)

XX DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1136.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX KW blood component; modification; succinimidy; maleimido group; amino;

XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents

XX PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 567; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)

XX CC comprising a therapeutically active amino acid region (III) and a

XX CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

XX CC a less therapeutically active amino acid region (IV), which covalently

XX CC bonds with amino/hydroxyl/thiol groups on blood components to form a

XX CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

XX CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 58; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDFLAEGGGVR 11
 |||||
 7 GDFLAEGGGVR 17

RESULT 15
 ABU09101
 ID ABU09101 standard; Peptide; 17 AA.
 XX AC ABU09101;
 XX DT 10-JUN-2003 (first entry)
 XX DE Alpha fibrinogen biopolymer peptide.
 XX KW Alpha fibrinogen; biopolymer; disease diagnosis; renal failure;
 XX KW intracerebral haemorrhage.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Optionally absent"
 FT Misc-difference 17 /note= "Optionally absent"
 FT Region 2..16
 FT /note= "This region is specifically claimed
 FT in claim 1 of the specification"
 XX US2002161179-A1.
 31-OCT-2002.

XX PF 30-APR-2001; 2001US-0845719.
 XX PR 30-APR-2001; 2001US-0845719.
 XX PA (JACK/) JACKOWSKI G.
 XX PA (THAT/) THATCHER B.
 XX PA (MARS/) MARSHALL J.
 XX PA (YANT/) YANTHA J.
 XX PA (VREE/) VREES T.
 XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
 XX WPI; 2003-340871/32.
 XX Biopolymer marker, useful in diagnosing disease states including renal
 PT failure and intracerebral hemorrhage, comprises Alpha Fibrinogen with a
 PT specified molecular weight -
 XX Disclosure; Fig 1; 10pp; English.

XX This invention relates to a novel biopolymer marker comprising an alpha
 CC fibrinogen peptide. The marker of the invention is useful in methods for
 CC diagnosing a disease state such as renal failure and/or intracerebral
 CC haemorrhage. Methods of the invention which use the alpha fibrinogen

CC peptide include mass spectroscopy or immunoassays, e.g.
 CC radioimmunoassay; enzyme-linked immunosorbent assay (ELISA) or
 CC fluorescent immunoassays. The invention allows characterisation of the
 CC presence or absence of a disease state relative to recognition of the
 CC presence or absence of the biopolymer. The present sequence represents
 CC an alpha fibrinogen biopolymer peptide sequence which may be used to
 CC characterise the presence or absence of a disease state such as renal
 CC failure or intracerebral haemorrhage.

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 58; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDFLAEGGGVR 11
 |||||
 6 GDFLAEGGGVR 16

Search completed: February 18, 2004, 16:25:49
 Job time : 42 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 16:22:15 ; Search time 21 seconds
(without alignments)
50.374 Million cell updates/sec

Title: US-09-846-342a-1_COPY_2_12
Perfect score: 58
Sequence: 1 GDFLAEGGVR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	16	2 C28854	fibrinopeptide A -
2	58	100.0	16	2 A24180	fibrinogen alpha c
3	58	100.0	16	2 B24180	fibrinogen alpha c
4	58	100.0	16	2 A28854	fibrinopeptide A -
5	58	100.0	16	2 B28854	fibrinopeptide A -
6	58	100.0	16	2 A29501	fibrinopeptide A -
7	58	100.0	644	1 FGHUA	fibrinogen alpha c
8	58	100.0	866	2 D44234	fibrinogen alpha c
9	54	93.1	17	2 E29501	fibrinopeptide A -
10	54	93.1	19	2 B29501	fibrinopeptide A -
11	54	93.1	19	2 C29501	fibrinopeptide A -
12	54	93.1	311	2 A05294	fibrinogen alpha c
13	52	89.7	15	2 F29501	fibrinopeptide A -
14	52	89.7	16	2 G29501	fibrinopeptide A -
15	52	89.7	16	2 H29501	fibrinogen alpha c
16	52	89.7	28	2 A05296	fibrinogen alpha c
17	49	84.5	15	2 I29501	fibrinopeptide A -
18	44	75.9	669	2 A72718	hypothetical prote
19	42	72.4	144	2 H84434	probable phloem-sp
20	42	72.4	223	2 B36506	hypothetical prote
21	40	69.0	280	2 H89800	hypothetical prote
22	40	69.0	863	2 A80525	outer membrane ush
23	39	67.2	199	2 AG1583	weakly phosphoglyc
24	39	67.2	271	2 S18730	aminoglycoside N3
25	39	67.2	324	2 D70943	hypothetical prote
26	39	67.2	1077	2 D90387	peptidase related
27	38	65.5	226	2 H84213	hypothetical prote
28	38	65.5	245	2 AG0701	Orf 245 protein [i
29	37	63.8	149	2 G85534	hypothetical prote

30 37 63.8 149 2 C90684 hypothetical prote
31 37 63.8 298 2 F87570 hypothetical prote
32 37 63.8 420 2 AD1295 phosphoribosylglyc
33 37 63.8 421 2 D69643 imidazolone-5-prop
34 37 63.8 607 2 B75071 tungsten-containin
35 37 63.8 607 2 F71094 probable aldehyde
36 36 62.1 153 2 T31968 hypothetical prote
37 36 62.1 156 2 H84251 flagella-related p
38 36 62.1 193 2 C75374 xanthine phosphori
39 36 62.1 246 2 E82832 3-methyl-2-oxobuta
40 36 62.1 399 2 G75610 imidazolonepropion
41 36 62.1 417 2 G84276 imidazolone-5-prop
42 36 62.1 507 1 F2WL L2 protein - human
43 36 62.1 558 2 S68981 aminonucleoside an
44 36 62.1 611 1 S12566 translation initia
45 36 62.1 627 2 AE2714 hypothetical prote

ALIGNMENTS

RESULT 1

C28854
fibrinopeptide A - gelada baboon
C;Species: Theropithecus gelada (gelada baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: C28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983

A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621

A;Accession: C28854

A;Molecule type: protein

A;Residues: 1-16 <NAK>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00076;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11

Db 6 GDFLAEGGVR 16

RESULT 2

A24180
fibrinogen alpha chain - Japanese macaque (fragment)
N;Contains: fibrinopeptide A

C;Species: Macaca fuscata (Japanese macaque)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
C;Accession: A24180

R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 97, 1487-1492, 1985

A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E

uenons, and baboons.

A;Reference number: A91990; MUID:85289140; PMID:3928610

A;Accession: A24180

A;Molecule type: protein

A;Residues: 1-16 <NAK>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00076;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11

Db 6 GDFLAEGGVR 16

RESULT 3

B24180

fibrinogen alpha chain - red guenon (fragment)
N:Contains: fibrinopeptide A
C:Species: Brythocebus patas (red guenon, hussar)
C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: B24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E. unenons, and baboons.
A:Reference number: A91990; MUID:85289140; PMID:3928610
A:Accession: B24180
A:Molecule type: protein
A:Residues: 1-16 <NAK>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
|||||
DB 6 GDFLAEGGGVR 16

RESULT 4
A28854
fibrinopeptide A - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C:Accession: A28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A>Title: Fibrinopeptides A and B of baboons (Papio anubis, and Theropit
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: A28854
A:Molecule type: protein
A:Residues: 1-16 <NAK>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
|||||
DB 6 GDFLAEGGGVR 16

RESULT 5
B28854
fibrinopeptide A - hamadryas baboon
C:Species: Papio hamadryas (hamadryas baboon)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C:Accession: B28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A>Title: Fibrinopeptides A and B of baboons (Papio anubis, and Theropit
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: B28854
A:Molecule type: protein
A:Residues: 1-16 <NAK>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
|||||
DB 6 GDFLAEGGGVR 16

RESULT 6
A28854
fibrinopeptide A - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C:Accession: A28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A>Title: Fibrinopeptides A and B of baboons (Papio anubis, and Theropit
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: A28854
A:Molecule type: protein
A:Residues: 1-16 <NAK>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
|||||
DB 6 GDFLAEGGGVR 16

RESULT 7
FGHUA
fibrinogen alpha chain precursor, short splice form [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide A
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C:Accession: A93956; A43568; A90468; I84456; A44234; C44234; B94433; B94309; S19
R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A>Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: ev
A:Reference number: A93956; MUID:83247396; PMID:6575389
A:Accession: A93956
A:Molecule type: mRNA
A:Residues: 1-644 <KAN>
A:Cross-references: GB:J00128; NID:g182425; PIDN:AAA52427.1; PID:g182426
A>Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Biol. 281, 39-48, 1990
A>Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; MUID:91344740; PMID:2102623
A:Accession: A43568
A:Molecule type: DNA
A:Residues: 1-330, 'A', 332-629 <CHU>
A:Cross-references: GB:M64982; NID:g182423; PIDN:AAA52426.1; PID:g182424
R:Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.
Biochemistry 22, 3237-3244, 1983
A>Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A:Reference number: A90468; MUID:83283432; PMID:6688355
A:Accession: A90468
A:Molecule type: mRNA
A:Residues: 1-330, 'A', 332-629 <RIX>
A:Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R:Rimam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A>Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains
A:Reference number: I37393; MUID:84069777; PMID:6689067
A:Accession: I84456
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 110-156 <RES>
A:Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A>Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A:Reference number: A44234; MUID:93090725; PMID:1457396
A:Accession: A44234
A:Molecule type: mRNA
A:Residues: 1-51 <FUL>
A:Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554

A29501
fibrinopeptide A - baboon
C:Species: Papio sp. (baboon)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C:Accession: A29501
R:Blombaek, B.; Blombaek, M.; Hann, C.
unpublished results, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: A29501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BLO>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 100.0%; Score 58; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
|||||
DB 6 GDFLAEGGGVR 16

A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918)
A;Accession: C44234
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 605-644 <FU2>
A;Cross-references: GB:M64982; NID:G458553; PIDN:AAAL7055.1; PID:G458554
A;Note: sequence extracted from NCBI backbone (NCBIP:119920)
R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in: *Protides of the Biological Fluids*, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Peeters, H., 1978
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A;Reference number: A94433
A;Accession: B94433
A;Molecule type: protein
A;Residues: 20-214, 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HEN>
R;Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlappin
A;Reference number: A90433; MUID:80088231; PMID:518846
A;Contents: disulfide bonds
A;Accession: A90433
A;Molecule type: protein
A;Residues: 20-145, 'Q', 148-195, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629
R;Tomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: variant, and disulfide bonds
A;Accession: B94309
A;Molecule type: protein
A;Residues: 20-65, 'T', 67-629 <BLO>
R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
Biochem. J. 281, 519-524, 1992
A;Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
incubation with calcium ionophore A23187.
A;Reference number: S19297; MUID:92143822; PMID:1736899
A;Accession: S19297
A;Molecule type: protein
A;Residues: 20-40 <DEW>
R;Retzius, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
A;Reference number: A60905; MUID:89162316; PMID:3232124
A;Accession: A60905
A;Molecule type: protein
A;Residues: 433-451 <RET>
R;Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
A;Reference number: A92225; MUID:78130085; PMID:632262
A;Contents: annotation; cross-linking acceptor sites
R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5403-5410, 1979
A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
A;Reference number: A90432; MUID:80088230; PMID:518845
A;Contents: annotation; cross-linking acceptor sites
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Icarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A;Title: Phosphorylation of fibrinogen by casein kinase 1.
A;Reference number: A90116; MUID:84104274; PMID:6318767
A;Contents: annotation; phosphorylation
A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylate
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986

A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; MUID:87057190; PMID:2877981
A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R;Krishnamurthi, S.; Dickens, T.A.; Patel, V.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote
A;Reference number: A33261; MUID:8932031; PMID:2783136
A;Contents: annotation; activity of cell attachment (R-G-D) motif
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te.
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haemeteria ghilianii, the giant South American leech.
R;Saenderker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep
Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an
A;Reference number: JC4334; MUID:96027996; PMID:7488038
A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptide.
C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:D44234 for the minor alternative splice form.
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: The list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see
ins are contained in the core. Two three-chain coiled coils emerge from this core and con
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-629/Product: fibrinogen alpha chain #status experimental <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-629/Product: fibrin alpha chain #status experimental <PGA>
F;36-38/Region: polymerization site, binding to the distal domain of the gamma chain of
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status i

Query Match 100.0%; Score 58; DB 1; Length 644;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11

Db 25 GDFLAEGGGVR 35

RESULT 8

D44234

fibrinogen alpha chain precursor, extended splice form - human

N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide A
C:Species: Homo sapiens (man)
C>Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
C:Accession: D44234; B44234
R:Pu, Y.; Weisbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A:Reference number: A44234; MUID:93090725; PMID:1457396
A:Accession: D44234
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA; DNA
A:Residues: 1-866 <FUI>
A:Cross-References: GB:M58569; NID:gl82406; PID:gl82407
A>Note: neither the complete nucleic acid sequence nor the complete translation are shown
A:Accession: B44234
A:Molecule type: mRNA; DNA
A:Residues: 605-866 <FUI>
A>Note: sequence extracted from NCBI backbone (NCBI:119917)
C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C:Genetics:
A:Gene: GDB:FGA
A:Cross-References: GDB:119129; OMIM:134820
A:Map position: 4q28-q28
A:Introns: 18/3; 60/3; 122/1; 171/2
A>Note: the list of introns is incomplete
C:Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
nained in the core. Two three-chain coiled coils emerge from this core and connect it
distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A:Pathway: blood coagulation
C:Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
F:1-19/Domains: signal sequence #status experimental
F:20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F:20-35/Product: fibrinopeptide A #status experimental <APT>
F:36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F:57-185/Domains: fibrinogen disulfide ring homology <FDR>
F:91-593/Region: cell attachment (R-G-D) motif
F:29-863/Domains: fibrinogen beta/gamma homology <FBG>
F:22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
F:55/Disulfide bonds: interchain (to beta-95) #status experimental
F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
F:68/Disulfide bonds: interchain (to gamma-106) #status experimental
F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
F:184/Disulfide bonds: interchain (to beta-223) #status experimental
F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F:461-491/Disulfide bonds: #status experimental
F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F:686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 58; DB 2; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11
| | | | | | | | | |
Db 25 GDFLAEGGGVR 35

RESULT 9

E29501
fibrinopeptide A - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: E29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: E29501
A:Molecule type: protein
A:Residues: 1-17 <BLO>
R:Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Contents: annotation; confirmation of species assignment
A:Reference number: A03118
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
Query Match 93.1%; Score 54; DB 2; Length 17;
Best Local Similarity 90.9%; Pred. No. 0.004;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
| | | | | | | | | |
Db 7 GEFLAEGGGVR 17

RESULT 10
E29501
fibrinopeptide A - European moose
C:Species: Alces alces alces (European moose, elk)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: B29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: B29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
Query Match 93.1%; Score 54; DB 2; Length 19;
Best Local Similarity 90.9%; Pred. No. 0.0045;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
| | | | | | | | | |
Db 9 GEFLAEGGGVR 19

RESULT 11
E29501
fibrinopeptide A - aoudad
C:Species: Ammotragus lervia (aoudad, Barbary sheep)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: C39501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: C29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
Query Match 93.1%; Score 54; DB 2; Length 19;
Best Local Similarity 90.9%; Pred. No. 0.0045;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDFLAEGGGVR 11
| | | | | | | | | |
Db 9 GEFLAEGGGVR 19

Query Match 93.1%; Score 54; DB 2; Length 19;
Best Local Similarity 90.9%; Pred. No. 0.0045;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11
| | | | | | | | | |
Db 9 GEFLAEGGGVR 19

Query Match 100.0%; Score 58; DB 2; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

A:Accession: F29501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BLO>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match      89.7%; Score 52; DB 2; Length 15;
Best Local Similarity 90.9%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GDFLAEGGGVR 11
      | | | | | | | |
Db      5 GSFLAEGGGVR 15

RESULT 14
G29501
fibrinopeptide A - bear
C:Species: Ursus sp. (bear)
C:Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C:Accession: G29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy
A:Reference number: A29501
A:Accession: G29501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen

Query Match      89.7%; Score 52; DB 2; Length 16;
Best Local Similarity 81.8%; Pred. No. 0.0085;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GDFLAEGGGVR 11
      | | | | | | | |
Db      6 GEFIAEGGGVR 16

RESULT 15
H29501
fibrinopeptide A - gray seal
C:Species: Halichoerus grypus (gray seal)
C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: H29501
R:Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy
A:Reference number: A29501
A:Accession: H29501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen

Query Match      89.7%; Score 52; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFLAEGGGVR 11
      | | | | | | | |
Db      7 DFLAEGGGVR 16

Search completed: February 18, 2004, 16:27:35
Job time : 22 secs

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Search completed: February 18, 2004, 16:27:35
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 16:04:10 ; Search time 11 seconds
(without alignments)

47.027 Million cell updates/sec

Title: US-09-846-342A-1_COPY_2_12
Perfect score: 58
Sequence: 1 GDFLAEGGVVR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	16	1 FIBA_MACFU	P12803 macaca fusc
2	58	100.0	19	1 FIBA_BISBO	P14441 bison bonas
3	58	100.0	866	1 FIBA_HUMAN	P02671 homo sapien
4	56	96.6	15	1 FIBA_CERSI	P14535 ceratotheri
5	54	93.1	15	1 FIBA_SYNCA	P14463 syncerus ca
6	54	93.1	16	1 FIBA_HYLLA	P14453 nyiobates l
7	54	93.1	16	1 FIBA_ODOHE	P14459 odocoileus
8	54	93.1	16	1 FIBA_TAPTE	P14536 tapirus ter
9	54	93.1	17	1 FIBA_PIG	P14460 sus scrofa
10	54	93.1	18	1 FIBA_CAMDR	P14444 camelus dro
11	54	93.1	18	1 FIBA_LAMGL	P14454 lama glama
12	54	93.1	19	1 FIBA_BUBBU	P14442 bubalus bub
13	54	93.1	19	1 FIBA_SHEEP	P14451 ovis aries
14	54	93.1	596	1 FIBA_BOVIN	P02672 bos taurus
15	52	89.7	16	1 FIBA_FELCA	P14450 felis silve
16	52	89.7	16	1 FIBA_MANLE	P14455 mandillus
17	52	89.7	19	1 FIBA_CEREL	P14446 cervus elap
18	52	89.7	28	1 FIBA_CANFA	P02673 canis fami
19	50	86.2	19	1 FIBA_MUNMU	P14457 mustiacus m
20	49	84.5	16	1 FIBA_EQUAS	P14449 equus asinu
21	48	82.8	14	1 FIBA_HORSE	P14452 equus cabal
22	48	82.8	19	1 FIBA_CERNI	P14447 cervus nipp
23	43	74.1	19	1 FIBA_RANTA	P14462 rangifer ta
24	41	70.7	271	1 PANB_XANAC	Q8p111 xanthomonas
25	41	70.7	271	1 PANB_XANCP	Q8p9t0 xanthomonas
26	39	67.2	271	1 AAC3_PSEAE	P29808 pseudomonas
27	37	63.8	420	1 PUR2_LISMO	Q8y6c6 listeria su
28	37	63.8	421	1 HUTI_BACSU	P42084 bacillus su
29	37	63.8	421	1 HUTI_STRP3	Q8k5m2 streptococc
30	37	63.8	421	1 HUTI_STRP8	Q8n253 streptococc
31	37	63.8	421	1 HUTI_STRP9	P58080 streptococc
32	37	63.8	607	1 AOR_FYRAB	Q9v035 pyrococcus
33	37	63.8	607	1 AOR_PYRHO	O58778 pyrococcus

RESULT 1	FIBA_MACFU	STANDARD;	PRT;	16 AA.
ID	FIBA_MACFU			
AC	P12803;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).			
GN	FGA.			
OS	Macaca fuscata fuscata (Japanese macaque),			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),			
OS	Macaca mulatta (Rhesus macaque),			
OS	Cercopithecus aethiops (Green monkey) (Griivet),			
OS	Erythrocebus patas (Red guenon) (Hussar),			
OS	Papio anubis (Olive baboon),			
OS	Papio hamadryas (Hamadryas baboon), and			
OS	Theropithecus gelada (Gelada baboon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=E.patas, and M.fuscata;			
RX	MEDLINE=85289140; PubMed=3928610;			
RA	Nakamura S., Takenaka O., Takahashi K.;			
RT	"Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and			
RT	patas monkey (Erythrocebus patas): their amino acid sequences,			
RT	restricted mutations, and a molecular phylogeny for macaques,			
RT	guenons, and baboons.";			
RL	J. Biochem. 97:1487-1492(1985).			
RN	[2]			
RP	SEQUENCE.			
RC	SPECIES=P.anubis, P.hamadryas, and T.gelada;			
RX	MEDLINE=84161822; PubMed=6423621;			
RA	Nakamura S., Takenaka O., Takahashi K.;			
RT	"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,			
RT	and Theropithecus gelada): their amino acid sequences and			
RT	evolutionary rates and a molecular phylogeny for the baboons.";			
RL	J. Biochem. 94:1973-1978(1983).			
RN	[3]			
RP	SEQUENCE.			
RC	SPECIES=C.aethiops, M.mulatta, and M.fascicularis;			
RX	Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;			
RA	"Studies on fibrinopeptides from primates.";			
RT	Acta Chem. Scand. 19:1788-1789(1965).			
RL	CC			
CC	-/- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT			
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET			
CC	AGGREGATION.			
CC	-/- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS			
CC	(ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-/- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY			
CC	THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA			
CC	CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES			
CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.			
DR	PIR; A24180; A24180.			

Q9kwu6 thermus aqu
Q9rz05 deinococcus
Q9hgq6 halobacteri
Q9rnk6 rhodobacter
P03105 human papil
P23588 homo sapien
P14445 cavia porce
P12801 anas platyr
Q10393 mycobacteri
P47256 mycoplasma
Q8why4 peilotum nu
P72848 synechocyst

ALIGNMENTS

SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
[12]
RN CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80089230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen."
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
[13]
RN CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human
fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).
[14]
RN VARIANT, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
[15]
RN REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
[16]
RN CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX MEDLINE=87057190; PubMed=2877981;
RA Kimura S., Aoki N.;
RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL J. Biol. Chem. 261:15591-15595(1986).
[17]
RN PHOSPHORYLATION.
RX MEDLINE=84104274; PubMed=6318767;
RA Icarte E., Plana M., Guasch M.D., Martos C.;
RT "Phosphorylation of fibrinogen by casein kinase 1.";
RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
[18]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX MEDLINE=92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha-chain of human
fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
[19]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX MEDLINE=97472408; PubMed=9332333;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
[20]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
[21]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX MEDLINE=98356117; PubMed=9689040;
RA Redman C., Doolittle R.F., Grieninger G.;
RT "Crystal structure of a recombinant alpha2E domain from human
fibrinogen-420.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
[22]
RN X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
[23]
RN VARIANT KYOTO-2.
RX MEDLINE=91300048; PubMed=2070049;
RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
characterized by the replacement of A alpha proline-18 by leucine.";
RL Blood 78:1149-1153(1991).
[24]
RN VARIANT LIMA.
RX MEDLINE=92340680; PubMed=1634621;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA Perez-Requejo J.L., Matsuda M.;
RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A
alpha-arginine-141 to serine substitution associated with extra
N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
formation but normal fibrin-facilitated plasminogen activation
catalyzed by tissue-type plasminogen activator.";
RL J. Clin. Invest. 90:67-76(1992).
[25]
RN VARIANT CARACAS-2.
RX MEDLINE=91268018; PubMed=1675636;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA Arocha-Pinango C.L., Matsuda M.;
RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
dysfibrinogen, fibrinogen Caracas II, characterized by impaired
fibrin gel formation.";
RL J. Biol. Chem. 266:11575-11581(1991).
[26]
RN VARIANT DUSART.
RX MEDLINE=93232289; PubMed=8473507;
RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
RA Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA Caen J.P.;
RT "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
its association with abnormal fibrin polymerization and
thrombophilia.";
Query Match 100.0%; Score 58; DB 1; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GDFLAEGGGVR 11
Db 25 GDFLAEGGGVR 35
RESULT 4
FIBA CERSI
ID FIBA CERSI STANDARD; PRT; 16 AA.
AC P14535;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RN SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

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CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1639 MW; 0958CBG6293F4C81 CRC64;

Query Match 96.6%; Score 56; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.0013;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11
   |:::|||||
   6 GDFLAEGGGVR 16

RESULT 5
FIBA SYNCA STANDARD; PRT; 15 AA.
AC P14453;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Syncerus caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Syncerus.
OX NCBI_TaxID=9970;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo.";
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
FT NON TER 15
SQ SEQUENCE 15 AA; 1480 MW; 4E998EASFOB41CC6 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 0.0027;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11
   |:::|||||
   5 GDFLAEGGGVR 15

RESULT 6
FIBA HYLLA STANDARD; PRT; 16 AA.
AC P14453;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

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GN FGA.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE.
RX MEDLINE=70294424; PubMed=5466708;
RA Moss G.A., Doolittle R.F., Roberts B.P.;
RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT at position B-3.";
RL Science 170:468-470(1970).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1565 MW; 49E98EB63EA04DD3 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGVR 11
   |:::|||||
   6 GDFLAEGGGVR 16

RESULT 7
FIBA ODOHE STANDARD; PRT; 16 AA.
AC P14459;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Odocoileus hemionus (Mule deer) (Black-tailed deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Odocoileus.
OX NCBI_TaxID=9872;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo.";
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1519 MW; E8098EB4B3B59C5 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GDFLAEGGVR 11
   |:|||||
Db 6 GEFLAEGGVR 16

RESULT 8
FIBA TAPTE
ID FIBA TAPTE STANDARD; PRT; 16 AA.
AC P14536;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9801;
RN [1]
RP SEQUENCE.
RQ O'Neil P.B., Doolittle R.F.;
   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
   RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW FIBRINOPEPTIDE A.
FT PEPTIDE 1 16
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1622 MW; 48598EB6292F4030 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11
   |:|||||
Db 6 GEFLAEGGVR 16

RESULT 9
FIBA PIG
ID FIBA PIG STANDARD; PRT; 17 AA.
AC P14460;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RQ Blomback B., Blomback M., Grondahl N.J.;
   "Studies on fibrinopeptides from mammals.";
   RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW FIBRINOPEPTIDE A.
FT PEPTIDE 1 17
FT NON TER 16 16
SQ SEQUENCE 17 AA; 1622 MW; 48598EB6292F4030 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.0029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11
   |:|||||
Db 6 GEFLAEGGVR 16

RESULT 10
FIBA CAMDR
ID FIBA CAMDR STANDARD; PRT; 18 AA.
AC P14444;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE.
RQ MEDLINE=67209145; PubMed=6033721;
   Doolittle R.F., Schubert D., Schwartz S.A.;
   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
   Dromedary camel, mule deer, and cape buffalo.";
   RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW FIBRINOPEPTIDE A.
FT PEPTIDE 1 18
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1835 MW; 244448763D7F4CC6 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 18;
Best Local Similarity 90.9%; Pred. No. 0.0032;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11
   |:|||||
Db 8 GEFLAEGGVR 18

RESULT 11
FIBA LAMGL
ID FIBA LAMGL STANDARD; PRT; 18 AA.
AC P14454;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Lama glama (Llama), and
   Lama vicugna (Vicugna) (Vicugna vicugna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844, 9843;

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[1]
RP SEQUENCE.
RC SPECIES=L.glamia;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
[2]
RP SEQUENCE.
RC SPECIES=L.vicugna;
RA Moss G.A., Doolittle R.F.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON TER 18
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4CC6 CRC64;
Query Match 93.1%; Score 54; DB 1; Length 18;
Best Local Similarity 90.9%; Pred. No. 0.0032;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GDFLAEGGGVR 11
Db 8 GEFLAEGGGVR 18
RESULT 12
FIBA_BUBBU
ID FIBA_BUBBU STANDARD; PRT; 19 AA.
AC P14442; P14443;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE.
RA Moss G.A., Doolittle R.F.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
[2]
RP SEQUENCE.
RC STRAIN=Italian breed;
RA Balestrieri C., Colonna G., Irace G.;
RT "Covalent structure of fibrinopeptides from buffaloes breeding in
Italy.";
RL Biochim. Biophys. Acta 405:517-521(1975).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 19 FIBRINOPEPTIDE A.

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FT VARIANT 8 8 S -> G (IN ITALIAN BRED).
FT NON TER 19
SQ SEQUENCE 19 AA; 1852 MW; 9BA41F0F55A54CC5 CRC64;
Query Match 93.1%; Score 54; DB 1; Length 19;
Best Local Similarity 90.9%; Pred. No. 0.0034;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GDFLAEGGGVR 11
Db 9 GEFLAEGGGVR 19
RESULT 13
FIBA_SHEEP
ID FIBA_SHEEP STANDARD; PRT; 19 AA.
AC P14451;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Ovis aries (Sheep), and
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 19 FIBRINOPEPTIDE A.
FT NON TER 19
SQ SEQUENCE 19 AA; 1848 MW; 99C98873D1B059C5 CRC64;
Query Match 93.1%; Score 54; DB 1; Length 19;
Best Local Similarity 90.9%; Pred. No. 0.0034;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GDFLAEGGGVR 11
Db 9 GEFLAEGGGVR 19
RESULT 14
FIBA_BOVIN
ID FIBA_BOVIN STANDARD; PRT; 596 AA.
AC P02672; O97642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 155-558 FROM N.A.
RA Murakawa M.;

```

Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

[2]
SEQUENCE OF 393-596 FROM N.A.
Chung D.W., Rixon M.W., Davie E.W.;
"The biosynthesis of fibrinogen and the cloning of its cDNA.";
(In) Bradshaw R.A. (eds.);
Proteins in biology and medicine, pp.309-328, Academic Press,
New York (1982).
[3]
SEQUENCE OF 1-19.
Sjoquist J., Blomback B., Wallen P.;
"Amino acid sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
[4]
SEQUENCE OF 1-19.
Folk J.E., Gladner J.A., Levin Y.;
"Thrombin-induced formation of co-fibrin. III. Acid degradation
studies and summary of sequential evidence on peptide A.";
J. Biol. Chem. 234:2317-2320(1959).
[5]
SEQUENCE OF 20-54.
MEDLINE=77112616; PubMed=836881;
Timpl R., Fietzek P.P., Wachter E., van Delden V.;
"Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II.
Isolation and sequence analysis of the chain constituents from the
amino terminal region.";
Biochim. Biophys. Acta 490:420-429(1977).
[6]
SEQUENCE OF 23-52.
MEDLINE=79164394; PubMed=434821;
Martinielli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
Hurrell J.G.R., Leach S.J., Scheraga H.A.;
"Amino acid sequences of portions of the alpha and beta chains of
bovine fibrinogen.";
Arch. Biochem. Biophys. 192:27-32(1979).
[7]
SEQUENCE OF 20-49; 243-268 AND 553-580.
Henschen A., Lottspeich F., Topfer-Petersen E., Kehl M., Timpl R.;
(In) Peeters H. (eds.);
Protides of the biological fluids, Proc. 28th colloquium, pp.47-50,
Pergamon Press, Oxford (1980).
[8]
X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 1-390.
MEDLINE=20087206; PubMed=10618375;
Brown J.H., Volkman N., Jun G., Henschen-Edman A.H., Cohen C.;
"The crystal structure of modified bovine fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 97:85-90(2000).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
ESTERON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
MONOMERS.

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CC EMBL; AF095463; AAC67562.1; .
DR PBL; 1DEQ; 15-NOV-99.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.

Blood coagulation; Plasma; Glycoprotein; Coiled coil; 3D-structure.
KW PEPTIDE 1 19
FT CHAIN 20 >596 FIBRINOPEPTIDE A.
FT DOMAIN 102 158 FIBRINOGEN ALPHA CHAIN.
FT DOMAIN 169 194 COILED COIL (POTENTIAL).
FT DOMAIN 429 432 COILED COIL (POTENTIAL).
FT DOMAIN 518 523 POLY-THR.
FT SITE 19 20 POLY-SER.
FT SITE 19 20 CLEAVAGE (BY THROMBIN; RELEASE
FIBRINOPEPTIDE A).
FT DISULFID 31 31 INTERCHAIN (WITH C-47') (BY SIMILARITY).
FT DISULFID 39 39 INTERCHAIN (WITH C-95 IN BETA) (BY
SIMILARITY).
FT DISULFID 48 48 INTERCHAIN (WITH C-49 IN GAMMA) (BY
SIMILARITY).
FT DISULFID 52 52 INTERCHAIN (WITH C-106 IN BETA) (BY
SIMILARITY).
FT DISULFID 164 164 INTERCHAIN (WITH C-165 IN GAMMA) (BY
SIMILARITY).
FT DISULFID 168 168 INTERCHAIN (WITH C-223 IN BETA) (BY
SIMILARITY).
FT DISULFID 436 466 BY SIMILARITY.
FT DISULFID 170 170 R -> K (IN REF. 1).
FT CONFLICT 207 208 IL -> LI (IN REF. 1).
FT CONFLICT 219 220 RE -> KK (IN REF. 1).
FT CONFLICT 341 353 MISSING (IN REF. 1).
FT CONFLICT 438 439 KV -> S (IN REF. 2).
FT NON TER 596 596
SQ SEQUENCE 596 AA; 65005 MW; 4B74118EF683A26A CRC64;
Query Match 93.1%; Score 54; DB 1; Length 596;
Best Local Similarity 90.9%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GDFLAEGGGVR 11
Db 9 GDFLTEGGVR 19
RESULT 15
FIBA_FELCA STANDARD; PRT; 16 AA.
ID FIBA_FELCA AC P14450;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;
Query Match 89.7%; Score 52; DB 1; Length 16;
Best Local Similarity 81.8%; Pred. No. 0.0063;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDFLAEGGVR 11
|:|:|:|:|:|:|
Db 6 GEFTAEGGVR 16

Search completed: February 18, 2004, 16:26:13
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 16:20:45 ; Search time 35 Seconds
(without alignments)
81.102 Million cell updates/sec

Title: US-09-846-342a-1_COPY_2_12
Perfect score: 58
Sequence: 1 GDFLAEGGVR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	218	4 Q8WW76	Q8WW76 homo sapien
2	51	87.9	557	11 Q99K47	Q99K47 mus musculus
3	44	75.9	669	17 Q9YFF9	Q9YFF9 aeropyrum p
4	42	72.4	144	10 Q9ZVR3	Q9ZVR3 arabidopsis
5	42	72.4	223	10 Q9C6Y9	Q9C6Y9 arabidopsis
6	41	70.7	184	16 Q92RY7	Q92RY7 rhizobium m
7	41	70.7	336	10 Q8LQ36	Q8LQ36 oryza sativ
8	40	69.0	280	16 Q99WM6	Q99WM6 staphylococ
9	40	69.0	280	16 Q8NY96	Q8NY96 staphylococ
10	40	69.0	863	16 Q8Z9C7	Q8Z9C7 salmonella
11	39	67.2	173	10 Q9FW83	Q9FW83 oryza sativ
12	39	67.2	199	16 Q92CG4	Q92CG4 listeria in
13	39	67.2	214	11 Q8RIE8	Q8RIE8 mus musculus
14	39	67.2	324	16 Q53481	Q53481 mycobacteri
15	39	67.2	481	10 Q8W0R4	Q8W0R4 sorghum bic
16	39	67.2	1077	17 Q97WN1	Q97WN1 sulfolobus

17	39	67.2	3010	12 Q81825	Q81825 hepatitis c
18	39	67.2	3010	12 Q68285	Q68285 hepatitis c
19	38	65.5	77	10 Q8W5N4	Q8W5N4 oryza sativ
20	38	65.5	147	10 Q9MAV0	Q9MAV0 arabidopsis
21	38	65.5	155	16 Q8ELS7	Q8ELS7 oceanobacil
22	38	65.5	186	2 Q9F7D5	Q9F7D5 salmonella
23	38	65.5	199	10 Q9FW52	Q9FW52 oryza sativ
24	38	65.5	226	17 Q9HRT2	Q9HRT2 halobacteri
25	38	65.5	245	16 Q8Z6K4	Q8Z6K4 salmonella
26	38	65.5	245	16 Q9Z4S4	Q9Z4S4 salmonella
27	38	65.5	268	2 Q84918	Q84918 thiobacillu
28	38	65.5	426	4 Q9GZT9	Q9GZT9 homo sapien
29	38	65.5	1458	12 Q8QTB8	Q8QTB8 white spot
30	38	65.5	2330	12 Q91L86	Q91L86 white spot
31	38	65.5	4180	12 Q8VAQ8	Q8VAQ8 white spot
32	37	63.8	125	2 Q9P9I9	Q9P9I9 comamonas
33	37	63.8	149	16 Q8XEA3	Q8XEA3 escherichia
34	37	63.8	256	16 Q92LM7	Q92LM7 rhizobium m
35	37	63.8	266	10 Q8GT14	Q8GT14 oryza sativ
36	37	63.8	298	16 Q9A571	Q9A571 caulobacter
37	37	63.8	328	5 Q8I702	Q8I702 trypanosoma
38	37	63.8	332	9 Q9MCA2	Q9MCA2 bacterioph
39	37	63.8	435	2 Q8GFN7	Q8GFN7 citrobacter
40	37	63.8	450	16 Q8P973	Q8P973 xanthomonas
41	37	63.8	547	10 Q8S9L5	Q8S9L5 arabidopsis
42	37	63.8	552	2 Q9APX1	Q9APX1 pseudomonas
43	37	63.8	564	4 Q8N1I1	Q8N1I1 homo sapien
44	37	63.8	577	10 Q9FLP1	Q9FLP1 arabidopsis
45	37	63.8	644	4 Q8NF84	Q8NF84 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8WW76	PRELIMINARY;	PRT;	218 AA.
AC	Q8WW76;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DE	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Similar to fibrinogen, A alpha polypeptide.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020764; AAH20764.1; -			
SQ	SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;			

Query Match 100.0%; Score 58; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GDFLAEGGVR 11
Db	25	GDFLAEGGVR 35

RESULT 2

ID	Q99K47	PRELIMINARY;	PRT;	557 AA.
AC	Q99K47;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)			
DE	Fibrinogen A alpha polypeptide..			
GN	FGA.			
OS	Mus musculus (Mouse).			

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005467; AAH05467.1; -.
DR HSSP; P02671; IFZA.
DR MGD; MGI:1316726; Fga.
SQ SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;

Query Match 87.9%; Score 51; DB 11; Length 557;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GDFLAEGGGV 11
   |:|:|:|:|:|
   26 GEFLSEGGGV 36

RESULT 3
Q9YFF9 PRELIMINARY; PRT; 669 AA.
AC Q9YFF9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein APE0283.
GN APE0283.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
   crenarchaeon, Aeropyrum pernix K1.";
   DNA Res. 6:83-101(1999).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 669 AA; 78475 MW; 926FB363E193BAE6 CRC64;

Query Match 75.9%; Score 44; DB 17; Length 669;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDFLAEGGGV 10
   |:|:|:|:|:|
   292 GEFLREGGGV 301

Db

RESULT 4
Q9ZVR3 PRELIMINARY; PRT; 144 AA.
AC Q9ZVR3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative phloem-specific lectin.
GN AT2G02280.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
   thaliana.";
   Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005312; AAC78511.1; -.
KW Lectin.
SQ SEQUENCE 144 AA; 16551 MW; 1B6E599C673D2A88 CRC64;

Query Match 72.4%; Score 42; DB 10; Length 144;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDFLAEGGGV 10
   |:|:|:|:|:|
   100 GEFLAEGGGV 109

Db

RESULT 5
Q9C6Y9 PRELIMINARY; PRT; 223 AA.
AC Q9C6Y9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 19.8 kDa protein.
GN T02313 OR T18F15.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., L.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Laing-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
   thaliana.";
   Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
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RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC T18F15 genomic sequence.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074228; AAG50547.1; -.
DR EMBL; AC084807; AAK43482.1; -.
DR InterPro; IPR002952; Eggshell.
DR PRINTS; PR01228; EGGSHLL.
KW Hypothetical protein.
SQ SEQUENCE 223 AA; 19781 MW; E21A0F404896897A CRC64;

Query Match 72.4%; Score 42; DB 10; Length 223;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDFLAEGGV 10
Db 69 GDFLGVGGV 78
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T 6
Q92RY7 PRELIMINARY; PRT; 184 AA.
AC Q92RY7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R00689.
GN R00689 OR SMC03071.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Gohier T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampegerger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591784; CAC45261.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 184 AA; 19500 MW; B3631AB7A878BC70 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 184;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDFLAEGGV 10
Db 123 GDVLAKGGI 132
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T 7
Q8LQ36 PRELIMINARY; PRT; 336 AA.
AC Q8LQ36
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ataxin 3-like protein.
GN P0529H1.24.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;

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RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0529H11.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004072; BAB92851.1; -.
DR Gramene; O8LQ36; -.
DR InterPro; IPR006155; Josephin.
DR Pfam; PF02099; Josephin; 1.
DR PRINTS; PR01233; JOSEPHIN.
SQ SEQUENCE 336 AA; 36204 MW; 84020FBEA78E8715 CRC64;

Query Match 70.7%; Score 41; DB 10; Length 336;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDFLAEGGV 9
Db 70 GDFLAEGGV 78
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RESULT 8
Q99WM6 PRELIMINARY; PRT; 280 AA.
ID Q99WM6
AC Q99WM6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SAV0351.
GN SAV0351 OR SA0339.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315);
RX MEDLINE=21311952; PubMed=1418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshina K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003359; BAB56513.1; -.
DR EMBL; AP003130; BAB41563.1; -.
DR InterPro; IPR003593; AAA_Arpase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 280 AA; 31464 MW; 2B0B9CF79F341652 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 280;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFLAEGGV 10
Db 176 DFVAQGGI 184
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RESULT 9
Q8NY96 PRELIMINARY; PRT; 280 AA.
ID Q8NY96
AC Q8NY96;

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DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE MW0327 protein.
GN MW0327.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12043378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naini T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
EMBL: AP004823; BAB94192.1; -.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
KW Complete proteome.
SQ SEQUENCE 280 AA; 31511 MW; 5AD98FDB4DF192B8 CRC64;
Query Match 69.0%; Score 40; DB 16; Length 280;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFLAEGGGV 10
DB 176 DFVAQGGGI 184
|||: |||:
Query Match 67.2%; Score 39; DB 10; Length 173;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GDFVLHGGGV 11
DB 25 GDEAASGGGVR 35
|||: |||:
RESULT 10
Q829C7 PRELIMINARY; PRT; 863 AA.
AC Q829C7
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Outer membrane usher protein HtrE.
GN STAC OR STV0205.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
EMBL: ALU67265; CAD01341.1; -.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW Complete proteome.
SQ SEQUENCE 863 AA; 94648 MW; C940F2B23409E736 CRC64;
Query Match 69.0%; Score 40; DB 16; Length 863;
Best Local Similarity 70.0%; Pred. No. 26+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GDFLAEGGGV 10
|||: |||:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE MW0327 protein.
GN MW0327.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12043378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naini T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
EMBL: AP004823; BAB94192.1; -.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
KW Complete proteome.
SQ SEQUENCE 280 AA; 31511 MW; 5AD98FDB4DF192B8 CRC64;
Query Match 69.0%; Score 40; DB 16; Length 280;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFLAEGGGV 10
DB 176 DFVAQGGGI 184
|||: |||:
Query Match 67.2%; Score 39; DB 10; Length 173;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GDFVLHGGGV 11
DB 25 GDEAASGGGVR 35
|||: |||:
RESULT 11
Q9FW83 PRELIMINARY; PRT; 173 AA.
AC Q9FW83
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical 18.8 kDa protein.
GN OSJNBA002612.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA002612 genomic sequence.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AC088924; AAG13511.1; -.
DR Gramene; Q9FW83; -.
KW Hypothetical protein.
SQ SEQUENCE 173 AA; 18795 MW; 3C324D9F64BC418A CRC64;
Query Match 67.2%; Score 39; DB 10; Length 173;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GDFVLHGGGV 11
DB 25 GDEAASGGGVR 35
|||: |||:
RESULT 12
Q92CG4 PRELIMINARY; PRT; 199 AA.
AC Q92CG4
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein lin1208.
GN LIN1208.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CLIP 11262 / Serovar 6a;
PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madsen E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
EMBL: AL596168; CAC96439.1; -.
DR ListiList; LIN01208; -.
DR InterPro; IPR001345; PG/BPGM_mutase.
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DR Pfam; PF00300; PGAM; 1.
KW PROSITE; PS00175; PG MUTASE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 199 AA; 22902 MW; E14DD962F4C6BFE5 CRC64;

Query Match 67.2%; Score 39; DB 16; Length 199;
Best Local Similarity 72.7%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GDFLAEGGVR 11
DB 102 GDFFAEYGGGR 112

RESULT 13
Q8RIE8 PRELIMINARY; PRT; 214 AA.
AC Q8RIE8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 22.6 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC024694; AAH24694.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 214 AA; 22606 MW; 41D6AC8803989DGE CRC64;

Query Match 67.2%; Score 39; DB 11; Length 214;
Best Local Similarity 63.6%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDFLAEGGVR 11
DB 185 GEWLGGGGLR 195

RESULT 14
O53481 PRELIMINARY; PRT; 324 AA.
AC O53481;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transmembrane protein.
GS RV2037C OR MT2097 OR MTV018.24C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T.C., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Braham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Emolaeva M., Salzberg S.L.,
RA Deicher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AL021899; CAA17251.1; -.
DR EMBL; AE007060; AAK46376.1; -.
DR TIGR; MT2097; -.
DR Tuberculist; RV2037c; -.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KW Transmembrane; Complete proteome.
FT CONFLICT 312 312 C -> Y (IN REF. 2).
SQ SEQUENCE 324 AA; 34688 MW; B8C8A4901E6D15FC CRC64;

Query Match 67.2%; Score 39; DB 16; Length 324;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DFLAEGGVR 11
DB 10 DLVCEGGVR 19

RESULT 15
Q8W0R4 PRELIMINARY; PRT; 481 AA.
AC Q8W0R4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative cytochrome P450-like protein.
GN SB32H17.4.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. BTx623;
RA Park Y.-J., Ramakrishna W., SanMiguel P., Emberton J., Bennetzen J.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. BTx623;
RA Liaca V., Young S., Kovchok S., Messing J.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF466201; AAL73972.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 481 AA; 54984 MW; 6145CFEFC0FD74FE CRC64;

Query Match 67.2%; Score 39; DB 10; Length 481;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DFLAEGGVR 11
DB 419 DFWAFGGGLR 428

Search completed: February 18, 2004, 16:27:02
Job time : 37 secs

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